



SEQUENCE LISTING

<110> Glass, David J.
Karow, Margaret
Smith, Eric

<120> HIV-Specific Fusion Proteins and
Therapeutic and Diagnostic Methods For Use

<130> REG 990A

<140> 10/768,932

<141> 2004-01-30

<150> US 60/446,347

<151> 2003-02-10

<160> 18

<170> FastSEQ for Windows Version 4.0

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<212> PRT

<213> Artificial Sequence

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<223> Synthetic

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Asp	Thr	Val	Glu	Leu	Thr	Cys	Thr	Ala	Ser	Gln	Lys	Lys	Ser	Ile	Gln
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Phe	His	Trp	Lys	Asn	Ser	Asn	Gln	Ile	Lys	Ile	Leu	Gly	Asn	Gln	Gly
65				70					75					80	
Ser	Phe	Leu	Thr	Lys	Gly	Pro	Ser	Lys	Leu	Asn	Asp	Arg	Ala	Asp	Ser
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Arg	Arg	Ser	Leu	Trp	Asp	Gln	Gly	Asn	Phe	Pro	Leu	Ile	Ile	Lys	Asn
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Leu	Lys	Ile	Glu	Asp	Ser	Asp	Thr	Tyr	Ile	Cys	Glu	Val	Glu	Asp	Gln
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Lys	Glu	Glu	Val	Gln	Leu	Leu	Val	Phe	Gly	Leu	Thr	Ala	Asn	Ser	Asp
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Thr	His	Leu	Leu	Gln	Gly	Gln	Ser	Leu	Thr	Leu	Thr	Leu	Glu	Ser	Pro
145				150					155						160
Pro	Gly	Ser	Ser	Pro	Ser	Val	Gln	Cys	Arg	Ser	Pro	Arg	Gly	Lys	Asn
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Ile	Gln	Gly	Gly	Lys	Thr	Leu	Ser	Val	Ser	Gln	Leu	Glu	Leu	Gln	Asp
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Ser	Gly	Thr	Trp	Thr	Cys	Thr	Val	Leu	Gln	Asn	Gln	Lys	Lys	Val	Glu

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Thr	Arg	Gly	Gly	Ala	Ile	Ala	Thr	Val	Glu	Leu	Thr	Cys	Thr	Ala	Ser		
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Gln	Lys	Lys	Ser	Ile	Gln	Phe	His	Trp	Lys	Asn	Ser	Asn	Gln	Ile	Lys		
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Asn	Asp	Arg	Ala	Asp	Ser	Arg	Arg	Ser	Leu	Trp	Asp	Gln	Gly	Asn	Phe		
			85					90					95				
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Cys	Glu	Val	Glu	Asp	Gln	Lys	Glu	Glu	Val	Gln	Leu	Leu	Val	Phe	Gly		
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Leu	Thr	Ala	Asn	Ser	Asp	Thr	His	Leu	Leu	Gln	Gly	Gln	Ser	Leu	Thr		
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Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr		
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Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn		
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Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro		
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Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln		
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Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val		
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Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val		
		355					360					365					
Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro		
	370					375					380						
Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr		
385					390					395					400		
Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val		
				405					410					415			
Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu		
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<212> PRT

<213> Artificial Sequence

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<223> Synthetic

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			20					25					30		
Thr	Arg	Gly	Gly	Ala	Ile	Ala	Lys	Val	Val	Leu	Gly	Lys	Lys	Gly	
		35					40					45			
Asp	Thr	Val	Glu	Leu	Thr	Cys	Thr	Ala	Ser	Gln	Lys	Lys	Ser	Ile	Gln
	50					55					60				
Phe	His	Trp	Lys	Asn	Ser	Asn	Gln	Ile	Lys	Ile	Leu	Gly	Asn	Gln	Gly
65					70					75					80
Ser	Phe	Leu	Thr	Lys	Gly	Pro	Ser	Lys	Leu	Asn	Asp	Arg	Ala	Asp	Ser
				85					90					95	
Arg	Arg	Ser	Leu	Trp	Asp	Gln	Gly	Asn	Phe	Pro	Leu	Ile	Ile	Lys	Asn
			100					105					110		
Leu	Lys	Ile	Glu	Asp	Ser	Asp	Thr	Tyr	Ile	Cys	Glu	Val	Glu	Asp	Gln
		115					120					125			
Lys	Glu	Glu	Val	Gln	Leu	Leu	Val	Phe	Gly	Leu	Thr	Ala	Asn	Ser	Asp
		130				135						140			
Thr	His	Leu	Leu	Gln	Gly	Gln	Ser	Leu	Thr	Leu	Thr	Leu	Glu	Ser	Pro
145					150					155					160
Pro	Gly	Ser	Ser	Pro	Ser	Val	Gln	Cys	Arg	Ser	Pro	Arg	Gly	Lys	Asn
				165					170					175	
Ile	Gln	Gly	Gly	Lys	Thr	Leu	Ser	Val	Ser	Gln	Leu	Glu	Leu	Gln	Asp
			180					185					190		
Ser	Gly	Thr	Trp	Thr	Cys	Thr	Val	Leu	Gln	Asn	Gln	Lys	Lys	Val	Glu
		195					200					205			
Phe	Lys	Ile	Asp	Ile	Val	Val	Leu	Ala	Ser	Gly	Phe	Gln	Lys	Ala	Ser
	210					215					220				
Ser	Ile	Val	Tyr	Lys	Lys	Glu	Gly	Glu	Gln	Val	Glu	Phe	Ser	Phe	Pro
225					230					235					240
Leu	Ala	Phe	Thr	Val	Glu	Lys	Leu	Thr	Gly	Ser	Gly	Glu	Leu	Trp	Trp
				245					250					255	
Gln	Ala	Glu	Arg	Ala	Ser	Ser	Ser	Lys	Ser	Trp	Ile	Thr	Phe	Asp	Leu
			260					265					270		
Lys	Asn	Lys	Glu	Val	Ser	Val	Lys	Arg	Val	Thr	Gln	Asp	Pro	Lys	Leu
		275					280					285			
Gln	Met	Gly	Lys	Lys	Leu	Pro	Leu	His	Leu	Thr	Leu	Pro	Gln	Ala	Leu
	290					295					300				
Pro	Gln	Tyr	Ala	Gly	Ser	Gly	Asn	Leu	Thr	Leu	Ala	Leu	Glu	Ala	Lys
305					310					315					320
Thr	Gly	Lys	Leu	His	Gln	Glu	Val	Asn	Leu	Val	Val	Met	Arg	Ala	Thr
				325					330					335	
Gln	Leu	Gln	Lys	Asn	Leu	Thr	Cys	Glu	Val	Trp	Gly	Pro	Thr	Ser	Pro
			340					345					350		
Lys	Leu	Met	Leu	Ser	Leu	Lys	Leu	Glu	Asn	Lys	Glu	Ala	Lys	Val	Ser
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Lys	Arg	Glu	Lys	Ala	Val	Trp	Val	Leu	Asn	Pro	Glu	Ala	Gly	Met	Trp
	370					375					380				
Gln	Cys	Leu	Leu	Ser	Asp	Gly	Ala	Ser	Gly	Asp	Lys	Thr	His	Thr	Cys
385					390					395					400

Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu
				405					410					415	
Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu
			420					425					430		
Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys
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Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys
	450					455					460				
Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu
465					470					475					480
Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys
				485					490					495	
Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys
			500					505					510		
Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser
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Arg	Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys
	530					535					540				
Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln
545					550					555					560
Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly
				565				570						575	
Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln
			580				585						590		
Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn
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<223> Synthetic

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			20					25					30		
Thr	Arg	Gly	Gly	Ala	Ile	Ala	Thr	Val	Glu	Leu	Thr	Cys	Thr	Ala	Ser
		35				40						45			
Gln	Lys	Lys	Ser	Ile	Gln	Phe	His	Trp	Lys	Asn	Ser	Asn	Gln	Ile	Lys
	50				55				60						
Ile	Leu	Gly	Asn	Gln	Gly	Ser	Phe	Leu	Thr	Lys	Gly	Pro	Ser	Lys	Leu
65				70					75						80
Asn	Asp	Arg	Ala	Asp	Ser	Arg	Arg	Ser	Leu	Trp	Asp	Gln	Gly	Asn	Phe
			85					90					95		
Pro	Leu	Ile	Ile	Lys	Asn	Leu	Lys	Ile	Glu	Asp	Ser	Asp	Thr	Tyr	Ile
			100				105						110		
Cys	Glu	Val	Glu	Asp	Gln	Lys	Glu	Glu	Val	Gln	Leu	Leu	Val	Phe	Gly
		115				120					125				
Leu	Thr	Ala	Asn	Ser	Asp	Thr	His	Leu	Leu	Gln	Gly	Gln	Ser	Leu	Thr
	130					135					140				

Leu	Thr	Leu	Glu	Ser	Pro	Pro	Gly	Ser	Ser	Pro	Ser	Val	Gln	Cys	Arg
145					150					155					160
Ser	Pro	Arg	Gly	Lys	Asn	Ile	Gln	Gly	Gly	Lys	Thr	Leu	Ser	Val	Ser
				165						170					175
Gln	Leu	Glu	Leu	Gln	Asp	Ser	Gly	Thr	Trp	Thr	Cys	Thr	Val	Leu	Gln
			180					185					190		
Asn	Gln	Lys	Lys	Val	Glu	Phe	Lys	Ile	Asp	Ile	Val	Val	Leu	Ala	Ser
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Gly	Phe	Gln	Lys	Ala	Ser	Ser	Ile	Val	Tyr	Lys	Lys	Glu	Gly	Glu	Gln
	210					215					220				
Val	Glu	Phe	Ser	Phe	Pro	Leu	Ala	Phe	Thr	Val	Glu	Lys	Leu	Thr	Gly
225					230					235					240
Ser	Gly	Glu	Leu	Trp	Trp	Gln	Ala	Glu	Arg	Ala	Ser	Ser	Ser	Lys	Ser
				245					250						255
Trp	Ile	Thr	Phe	Asp	Leu	Lys	Asn	Lys	Glu	Val	Ser	Val	Lys	Arg	Val
			260					265					270		
Thr	Gln	Asp	Pro	Lys	Leu	Gln	Met	Gly	Lys	Lys	Leu	Pro	Leu	His	Leu
		275					280						285		
Thr	Leu	Pro	Gln	Ala	Leu	Pro	Gln	Tyr	Ala	Gly	Ser	Gly	Asn	Leu	Thr
	290					295					300				
Leu	Ala	Leu	Glu	Ala	Lys	Thr	Gly	Lys	Leu	His	Gln	Glu	Val	Asn	Leu
305					310					315					320
Val	Val	Met	Arg	Ala	Thr	Gln	Leu	Gln	Lys	Asn	Leu	Thr	Cys	Glu	Val
				325					330					335	
Trp	Gly	Pro	Thr	Ser	Pro	Lys	Leu	Met	Leu	Ser	Leu	Lys	Leu	Glu	Asn
			340					345					350		
Lys	Glu	Ala	Lys	Val	Ser	Lys	Arg	Glu	Lys	Ala	Val	Trp	Val	Leu	Asn
	355						360					365			
Pro	Glu	Ala	Gly	Met	Trp	Gln	Cys	Leu	Leu	Ser	Asp	Gly	Ala	Ser	Gly
	370					375					380				
Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly
385					390					395					400
Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met
				405					410					415	
Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His
			420					425					430		
Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val
		435					440					445			
His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr
	450					455					460				
Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly
465					470					475					480
Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile
				485					490					495	
Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val
		500						505					510		
Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser
	515						520					525			
Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu
	530					535					540				
Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro
545					550					555					560
Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val
				565					570					575	
Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met
			580					585					590		
His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser

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Pro Gly Lys
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600

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<210> 6
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<213> Artificial Sequence

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<400> 6

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			20					25					30		
Thr	Arg	Asp	Tyr	Gln	Val	Ser	Ser	Pro	Ile	Tyr	Asp	Ile	Asn	Tyr	Tyr
	35						40					45			
Thr	Ser	Glu	Pro	Ser	Gln	Lys	Ile	Asn	Val	Lys	Gln	Ile	Ala	Ala	Arg
	50					55					60				
Leu	Leu	Ala	Ile	Ala	Lys	Lys	Val	Val	Leu	Gly	Lys	Lys	Gly	Asp	Thr
65					70					75					80
Val	Glu	Leu	Thr	Cys	Thr	Ala	Ser	Gln	Lys	Lys	Ser	Ile	Gln	Phe	His
				85					90					95	
Trp	Lys	Asn	Ser	Asn	Gln	Ile	Lys	Ile	Leu	Gly	Asn	Gln	Gly	Ser	Phe
			100					105					110		
Leu	Thr	Lys	Gly	Pro	Ser	Lys	Leu	Asn	Asp	Arg	Ala	Asp	Ser	Arg	Arg
	115					120						125			
Ser	Leu	Trp	Asp	Gln	Gly	Asn	Phe	Pro	Leu	Ile	Ile	Lys	Asn	Leu	Lys
	130					135						140			
Ile	Glu	Asp	Ser	Asp	Thr	Tyr	Ile	Cys	Glu	Val	Glu	Asp	Gln	Lys	Glu
145					150					155					160
Glu	Val	Gln	Leu	Leu	Val	Phe	Gly	Leu	Thr	Ala	Asn	Ser	Asp	Thr	His
				165					170					175	
Leu	Leu	Gln	Gly	Gln	Ser	Leu	Thr	Leu	Thr	Leu	Glu	Ser	Pro	Pro	Gly
			180					185					190		
Ser	Ser	Pro	Ser	Val	Gln	Cys	Arg	Ser	Pro	Arg	Gly	Lys	Asn	Ile	Gln
	195					200						205			
Gly	Gly	Lys	Thr	Leu	Ser	Val	Ser	Gln	Leu	Glu	Leu	Gln	Asp	Ser	Gly
	210					215						220			
Thr	Trp	Thr	Cys	Thr	Val	Leu	Gln	Asn	Gln	Lys	Lys	Val	Glu	Phe	Lys
225					230					235					240
Ile	Asp	Ile	Val	Val	Leu	Ala	Ser	Gly	Asp	Lys	Thr	His	Thr	Cys	Pro
				245					250					255	
Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe
			260					265					270		
Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val
	275					280						285			
Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe
	290					295					300				
Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro
305					310					315					320
Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr
				325					330					335	
Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val

				340				345					350				
Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala		
		355					360						365				
Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg		
		370					375					380					
Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly		
385					390					395					400		
Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro		
				405					410					415			
Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser		
			420					425					430				
Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln		
		435					440					445					
Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His		
	450					455					460						
Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys						
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<400> 7

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Glu	Pro	Ser	Gln	Lys	Ile	Asn	Val	Lys	Gln	Ile	Ala	Ala	Arg	Leu	Leu		
			20					25					30				
Thr	Arg	Gly	Gly	Ala	Ile	Ala	Lys	Val	Val	Leu	Gly	Lys	Lys	Gly			
		35					40				45						
Asp	Thr	Val	Glu	Leu	Thr	Cys	Thr	Ala	Ser	Gln	Lys	Lys	Ser	Ile	Gln		
	50					55					60						
Phe	His	Trp	Lys	Asn	Ser	Asn	Gln	Ile	Lys	Ile	Leu	Gly	Asn	Gln	Gly		
65				70					75						80		
Ser	Phe	Leu	Thr	Lys	Gly	Pro	Ser	Lys	Leu	Asn	Asp	Arg	Ala	Asp	Ser		
				85					90					95			
Arg	Arg	Ser	Leu	Trp	Asp	Gln	Gly	Asn	Phe	Pro	Leu	Ile	Ile	Lys	Asn		
			100					105					110				
Leu	Lys	Ile	Glu	Asp	Ser	Asp	Thr	Tyr	Ile	Cys	Glu	Val	Glu	Asp	Gln		
		115					120					125					
Lys	Glu	Glu	Val	Gln	Leu	Leu	Val	Phe	Gly	Leu	Thr	Ala	Asn	Ser	Asp		
	130					135					140						
Thr	His	Leu	Leu	Gln	Gly	Gln	Ser	Leu	Thr	Leu	Thr	Leu	Glu	Ser	Pro		
145				150					155						160		
Pro	Gly	Ser	Ser	Pro	Ser	Val	Gln	Cys	Arg	Ser	Pro	Arg	Gly	Lys	Asn		
				165				170						175			
Ile	Gln	Gly	Gly	Lys	Thr	Leu	Ser	Val	Ser	Gln	Leu	Glu	Leu	Gln	Asp		
		180						185					190				
Ser	Gly	Thr	Trp	Thr	Cys	Thr	Val	Leu	Gln	Asn	Gln	Lys	Lys	Val	Glu		
	195					200						205					
Phe	Lys	Ile	Asp	Ile	Val	Val	Leu	Ala	Ser	Gly	Asp	Lys	Thr	His	Thr		
	210					215					220						
Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe		

225					230					235					240
Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro
				245					250					255	
Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val
			260					265					270		
Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr
		275					280					285			
Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val
	290					295					300				
Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys
305					310					315					320
Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser
			325						330					335	
Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro
			340				345						350		
Ser	Arg	Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val
		355				360						365			
Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly
	370					375					380				
Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp
385					390				395						400
Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp
			405					410					415		
Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His
			420					425				430			
Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys	Ala	Ser
		435				440					445				
Ala	Asp	Tyr	Gln	Val	Ser	Ser	Pro	Ile	Tyr	Asp	Ile	Asn	Tyr	Tyr	Thr
	450				455				460						
Ser	Glu	Pro	Ser	Gln	Lys	Ile	Asn	Val	Lys	Gln	Ile	Ala	Ala	Arg	Leu
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<211> 453

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 8

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Lys	Gly	Asp	Thr	Val	Glu	Leu	Thr	Cys	Thr	Ala	Ser	Gln	Lys	Lys	Ser
		20						25				30			
Ile	Gln	Phe	His	Trp	Lys	Asn	Ser	Asn	Gln	Ile	Lys	Ile	Leu	Gly	Asn
		35				40					45				
Gln	Gly	Ser	Phe	Leu	Thr	Lys	Gly	Pro	Ser	Lys	Leu	Asn	Asp	Arg	Ala
	50					55				60					
Asp	Ser	Arg	Arg	Ser	Leu	Trp	Asp	Gln	Gly	Asn	Phe	Pro	Leu	Ile	Ile
65				70					75					80	
Lys	Asn	Leu	Lys	Ile	Glu	Asp	Ser	Asp	Thr	Tyr	Ile	Cys	Glu	Val	Glu
			85					90					95		
Asp	Gln	Lys	Glu	Glu	Val	Gln	Leu	Leu	Val	Phe	Gly	Leu	Thr	Ala	Asn

			100					105				110					
Ser	Asp	Thr	His	Leu	Leu	Gln	Gly	Gln	Ser	Leu	Thr	Leu	Thr	Leu	Glu		
		115					120					125					
Ser	Pro	Pro	Gly	Ser	Ser	Pro	Ser	Val	Gln	Cys	Arg	Ser	Pro	Arg	Gly		
		130				135					140						
Lys	Asn	Ile	Gln	Gly	Gly	Lys	Thr	Leu	Ser	Val	Ser	Gln	Leu	Glu	Leu		
145				150						155				160			
Gln	Asp	Ser	Gly	Thr	Trp	Thr	Cys	Thr	Val	Leu	Gln	Asn	Gln	Lys	Lys		
			165						170					175			
Val	Glu	Phe	Lys	Ile	Asp	Ile	Val	Val	Leu	Ala	Ser	Gly	Asp	Lys	Thr		
		180					185					190					
His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser		
		195				200						205					
Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg		
	210					215					220						
Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro		
225				230					235						240		
Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala		
			245						250					255			
Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val		
		260					265					270					
Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr		
		275				280					285						
Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr		
	290				295				300								
Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu		
305				310					315						320		
Pro	Pro	Ser	Arg	Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys		
			325					330						335			
Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser		
		340					345					350					
Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp		
	355					360					365						
Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser		
	370				375						380						
Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala		
385				390					395						400		
Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys		
			405					410						415			
Ala	Ser	Ala	Asp	Tyr	Gln	Val	Ser	Ser	Pro	Ile	Tyr	Asp	Ile	Asn	Tyr		
		420					425				430						
Tyr	Thr	Ser	Glu	Pro	Ser	Gln	Lys	Ile	Asn	Val	Lys	Gln	Ile	Ala	Ala		
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Arg	Leu	Leu	Ser	Arg													
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<220>
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			20					25					30			
Thr	Arg	Gly	Gly	Ala	Ile	Ala	Lys	Lys	Val	Val	Leu	Gly	Lys	Lys	Gly	
		35					40					45				
Asp	Thr	Val	Glu	Leu	Thr	Cys	Thr	Ala	Ser	Gln	Lys	Lys	Ser	Ile	Gln	
	50					55					60					
Phe	His	Trp	Lys	Asn	Ser	Asn	Gln	Ile	Lys	Ile	Leu	Gly	Asn	Gln	Gly	
65				70					75						80	
Ser	Phe	Leu	Thr	Lys	Gly	Pro	Ser	Lys	Leu	Asn	Asp	Arg	Ala	Asp	Ser	
				85				90						95		
Arg	Arg	Ser	Leu	Trp	Asp	Gln	Gly	Asn	Phe	Pro	Leu	Ile	Ile	Lys	Asn	
			100					105					110			
Leu	Lys	Ile	Glu	Asp	Ser	Asp	Thr	Tyr	Ile	Cys	Glu	Val	Glu	Asp	Gln	
		115					120					125				
Lys	Glu	Glu	Val	Gln	Leu	Leu	Val	Phe	Gly	Leu	Thr	Ala	Asn	Ser	Asp	
		130			135						140					
Thr	His	Leu	Leu	Gln	Gly	Gln	Ser	Leu	Thr	Leu	Thr	Leu	Glu	Ser	Pro	
145				150					155						160	
Pro	Gly	Ser	Ser	Pro	Ser	Val	Gln	Cys	Arg	Ser	Pro	Arg	Gly	Lys	Asn	
				165				170						175		
Ile	Gln	Gly	Gly	Lys	Thr	Leu	Ser	Val	Ser	Gln	Leu	Glu	Leu	Gln	Asp	
		180					185						190			
Ser	Gly	Thr	Trp	Thr	Cys	Thr	Val	Leu	Gln	Asn	Gln	Lys	Lys	Val	Glu	
		195					200					205				
Phe	Lys	Ile	Asp	Ile	Val	Val	Leu	Ala	Ser	Gly	Asp	Lys	Thr	His	Thr	
	210				215						220					
Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	
225				230					235						240	
Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	
				245				250						255		
Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	
		260					265						270			
Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	
		275					280					285				
Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	
	290					295					300					
Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	
305				310						315					320	
Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	
				325				330						335		
Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	
			340				345						350			
Ser	Arg	Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	
		355				360						365				
Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	
	370					375					380					
Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	
385				390					395						400	
Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	
				405				410						415		
Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	
			420					425					430			
Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys			
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aatccggaag ctagcaccac gatgtc 26

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tccggattcc agaaggcctc cagcatagtc 30

<210> 14
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<220>
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<400> 16
caaacgcgtc aggaggcggg ctgcgatttg 30

<210> 17
<211> 61
<212> DNA
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<220>
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<400> 17
gggaagctgt acaggtcagt tccactgtag cgatcgctcc accacgcgtc aggaggcggg 60
c 61

<210> 18
<211> 61
<212> DNA
<213> Artificial Sequence

<220>
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<400> 18
gcccgcctcc tgacgcgtgg tggagcgatc gctacagtgg aactgacctg tacagcttcc 60
c 61